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SEQUENCE LISTING

<110> MENOZZI, Franco
LOCHT, Camille

<120> IDENTIFICATION AND CLONING OF A MYCOBACTERIAL ANTIGEN
CORRESPONDING TO A HEPARIN-BINDING HAEMAGGLUTININ

<130> 960-34

<140> 09/192,579

<141> 1998-11-17

<150> FR 96 06168

<151> 1996-05-17

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 39

<212> PRT

<213> Mycobacterium

<220>

<223> sequence comprising a region involved in
interactions with sulphated glycoconjugates and in
heparin binding

<400> 1

Lys Lys Ala Ala Pro Ala Lys Lys Ala Ala Pro Ala Lys Lys Ala Ala
1 5 10 15

Pro Ala Lys Lys Ala Ala Ala Lys Lys Ala Pro Ala Lys Lys Ala Ala
20 25 30

Ala Lys Lys Val Thr Gln Lys
35

<210> 2

<211> 10

<212> PRT

<213> Mycobacterium

<220>

<223> peptide S1441

<400> 2

Lys Ala Glu Gly Tyr Leu Glu Ala Ala Thr
1 5 10

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<210> 3
<211> 18
<212> PRT
<213> Mycobacterium

<220>
<221> CDS
<222> (1)
<223> peptide S1443; Xaa can be any amino acid

<400> 3
Xaa Glu Gly Tyr Val Asp Gln Ala Val Glu Leu Thr Gln Glu Ala Leu
1 5 10 15

Gly Lys

<210> 4
<211> 9
<212> PRT
<213> Mycobacterium

<220>
<221> CDS
<222> (1), (4) and (8)
<223> peptide S1446; Xaa can be any amino acid

<400> 4
Xaa Gln Glu Xaa Leu Pro Glu Xaa Leu
1 5

<210> 5
<211> 7
<212> PRT
<213> Mycobacterium

<220>
<223> Peptide S1447

<400> 5
Phe Thr Ala Glu Glu Leu Arg
1 5

<210> 6
<211> 17
<212> DNA
<213> Mycobacterium

<220>
<223> Oligonucleotide originated from the S1441 peptide
(oligo S1441)

<400> 6
aaggcsgagg gstacct

<210> 7
<211> 17
<212> DNA
<213> Mycobacterium

<220>
<223> Oligonucleotide originated from the S1441 peptide
(reverse oligo S1441)

<400> 7
aggtascct csgcctt

17

<210> 8
<211> 17
<212> DNA
<213> Mycobacterium

<220>
<223> Oligonucleotide originated from the S1443 peptide
(oligo S1443)

<400> 8
gaccaggcsg tsgagct

17

<210> 9
<211> 17
<212> DNA
<213> Mycobacterium

<220>
<223> Oligonucleotide originated from the S1443 peptide
(reverse oligo S1443)

<400> 9
agctcsacsg cctggctc

17

<210> 10
<211> 21
<212> DNA
<213> Mycobacterium

<220>
<223> Oligonucleotide named HBHASEq1 and used for
sequencing the gene coding for HBHA

<400> 10
agccggtaca acgagctggt c

21

<210> 11
<211> 21
<212> DNA

<213> Mycobacterium

<220>

<223> Oligonucleotide named HBHA Seq1inv and used for
sequencing the gene coding for HBHA

<400> 11

gaccagctcg ttgtaccggc t

21

<210> 12

<211> 19

<212> DNA

<213> Mycobacterium

<220>

<223> Oligonucleotide named HBHASEq2 and used for
sequencing the gene coding for HBHA

<400> 12

catccaacac gtcgactcc

19

<210> 13

<211> 19

<212> DNA

<213> Mycobacterium

<220>

<223> Oligonucleotide named HBHA Seq3 and used for
sequencing the gene coding for HBHA

<400> 13

ttgatgtcat caatgttcg

19

<210> 14

<211> 19

<212> DNA

<213> Mycobacterium

<220>

<223> Oligonucleotide named HBHA Seq4 and used for
sequencing the gene coding for HBHA

<400> 14

cgtggaccag gcggtggag

19

<210> 15

<211> 21

<212> DNA

<213> Mycobacterium

<220>

<223> Oligonucleotide named HBHA Seq 5 and used for
sequencing the gene coding for HBHA

<400> 15
gacgatcagg aggtttcccc g 21

<210> 16
<211> 24
<212> DNA
<213> Mycobacterium

<220>
<223> Oligonucleotide named reverse primer and used for
sequencing the gene coding for HBHA

<400> 16
agcggataac aatttcacac agga 24

<210> 17
<211> 149
<212> DNA
<213> Mycobacterium

<220>
<223> nucleotide sequence and amino sequence of a fragment of HBHA
deduced from a PCR fragment of chromosomal BCG DNA

<220>
<221> CDS
<222> (1)..(147)

<400> 17
aag gcc gag ggc tac ctc gag gcc gcg act agc cgg tac aac gag ctg 48
Lys Ala Glu Gly Tyr Leu Glu Ala Ala Thr Ser Arg Tyr Asn Glu Leu
1 5 10 15
gtc gag cgc ggt gag gcc gct cta gag cgg ctg cgc agc cag cag agc 96
Val Glu Arg Gly Glu Ala Ala Leu Glu Arg Leu Arg Ser Gln Gln Ser
20 25 30
ttc gag gaa gtg tcg gcg ccc gcc gaa ggc tac gtg gac cag gcg gtc 144
Phe Glu Glu Val Ser Ala Pro Ala Glu Gly Tyr Val Asp Gln Ala Val
35 40 45
gag ct 149
Glu

<210> 18
<211> 49
<212> PRT
<213> Mycobacterium
<223> amino sequence of a fragment of HBHA deduced from a
PCR fragment of chromosomal BCG DNA

<400> 18

Lys Ala Glu Gly Tyr Leu Glu Ala Ala Thr Ser Arg Tyr Asn Glu Leu
1 5 10 15

Val Glu Arg Gly Glu Ala Ala Leu Glu Arg Leu Arg Ser Gln Gln Ser
20 25 30

Phe Glu Glu Val Ser Ala Pro Ala Glu Gly Tyr Val Asp Gln Ala Val
35 40 45

Glu

<210> 19

<211> 1097

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
of the BCG gene coding for HBHA

<220>

<221> CDS

<222> (331)..(924)

<223> CDS from 811 to 828, from 829 to 846, from 847 to
864, from 865 to 885 and from 895 to 915 : peptide
which may be particularly involved in interactions
with sulphated glycoconjugates

<400> 19

cggctggcgg gtaatcaaac ctgaaggaca gtcattctggg tgaggctcgac cgcaggctga 60
tccagccgat cggccggcgc tggccaacag cgactccgtc gatgacgtgc agcaaaggag 120
acatgtagt accggatcag ctgggcctga catctacgaa ctcgaccgac aaccgacccg 180
acgatcagga ggtttccccg gcaagtcgcg tgccatgtca atccgcgggt cttgactagt 240
cctccctgga ggagccgacg cttgccccaa cgtccagacc aaagatgtaa gaacgccgat 300
atcagaaaat agttaatgaa aggaataccc atg gct gaa aac tcg aac att gat 354
Met Ala Glu Asn Ser Asn Ile Asp
1 5
gac atc aag gct ccg ttg ctt gcc gcg ctt gga gcg gcc gac ctg gcc 402
Asp Ile Lys Ala Pro Leu Leu Ala Ala Leu Gly Ala Ala Asp Leu Ala
10 15 20
ttg gcc act gtc aac gag ttg atc acg aac ctg cgt gag cgt gcg gag 450
Leu Ala Thr Val Asn Glu Leu Ile Thr Asn Leu Arg Glu Arg Ala Glu
25 30 35 40
gag act cgt acg gac acc cgc agc cgg gtc gag gag agc cgt gct cgc 498
Glu Thr Arg Thr Asp Thr Arg Ser Arg Val Glu Glu Ser Arg Ala Arg
45 50 55

Thr Asn Leu Arg Glu Arg Ala Glu Glu Thr Arg Thr Asp Thr Arg Ser
 35 40 45
 Arg Val Glu Glu Ser Arg Ala Arg Leu Thr Lys Leu Gln Glu Asp Leu
 50 55 60
 Pro Glu Gln Leu Thr Glu Leu Arg Glu Lys Phe Thr Ala Glu Glu Leu
 65 70 75 80
 Arg Lys Ala Ala Glu Gly Tyr Leu Glu Ala Ala Thr Ser Arg Tyr Asn
 85 90 95
 Glu Leu Val Glu Arg Gly Glu Ala Ala Leu Glu Arg Leu Arg Ser Gln
 100 105 110
 Gln Ser Phe Glu Glu Val Ser Ala Pro Ala Glu Gly Tyr Val Asp Gln
 115 120 125
 Ala Val Glu Leu Thr Gln Glu Ala Leu Gly Thr Val Ala Ser Gln Thr
 130 135 140
 Arg Ala Val Gly Glu Arg Ala Ala Lys Leu Val Gly Ile Glu Leu Pro
 145 150 155 160
 Lys Lys Ala Ala Pro Ala Lys Lys Ala Ala Pro Ala Lys Lys Ala Ala
 165 170 175
 Pro Ala Lys Lys Ala Ala Ala Lys Lys Ala Pro Ala Lys Lys Ala Ala
 180 185 190
 Ala Lys Lys Val Thr Gln
 195